What is claimed is:

1. A method of identifying one or more markers for cancer, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having cancer, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for cancer; and

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals not having cancer,

wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being markers for cancer.

2. A method of identifying one or more markers for cancer, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having cancer, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for cancer; and

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals having cancer,

wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being markers for cancer.

3. A method of identifying one or more markers of a stage of cancer progression or regression, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of cancer, wherein said one or more individuals are at the same progressive or regressive stage of cancer, and wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for determining the stage of progression or regression of cancer, and;

b) comparing the level of each of said one or more gene transcripts from said step a)

with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of cancer distinct from that of said one or more individuals of step a),

wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being markers for the stage of progression or regression of cancer.

4. A method of identifying one or more markers of a stage of cancer progression or regression, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of cancer, wherein said one or more individuals are at the same progressive or regressive stage of cancer, and wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for determining the stage of progression or regression of cancer, and;

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of cancer identical to that of said one or more individuals of step a),

wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being markers for the stage of progression or regression of cancer.

5. The method of any one of claims 1 - 4, wherein each of said one or more markers identifies one or more transcripts of one or more non immune response genes.

6. The method of any one of claims 1 - 4, wherein each of said one or more markers identifies a transcript of a gene expressed by non-blood tissue.

7. The method of any one of claims 1 - 4, wherein each of said one or more markers identifies a transcript of a gene expressed by non-lymphoid tissue.

8. The method of any one of claims 1 - 4, wherein said cancer is selected from the group consisting of liver cancer, bladder cancer, colon cancer, lung cancer, leukemia, ovarian cancer, cervical cancer, gastric cancer, kidney cancer, brain cancer, prostate cancer, pancreatic cancer, nasopharyngeal cancer, and breast cancer.

9. The method of claim 8 wherein said cancer is non-metastatic.

10. The method of any one of claims 1 - 4, wherein each of said one or more markers identifies a transcript of a gene selected from the group consisting of the genes listed in Table 3J, Table 3K and Table 3X.

11. A method of diagnosing or prognosing cancer in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual, wherein said one or more gene transcripts corresponds to said one or more markers of claim 1 and claim 2, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having cancer,

wherein detecting a difference in the levels of each of said one or more gene transcripts in the comparison of step b) is indicative of cancer in the individual of step a).

12. A method of diagnosing or prognosing cancer in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual, wherein said one or more gene transcripts corresponds to said one or more markers of claim 1 and claim 2, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having cancer,

wherein detecting the same levels of each of said one or more gene transcripts in the comparison of step b) is indicative of cancer in the individual of step a).

13. A method of determining a stage of disease progression or regression in an individual having cancer, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual having cancer, wherein said one or more gene transcripts corresponds to said one or more markers of claim 3 and claim 4, and

b) comparing the level of each if said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood obtained from one or more individuals who each have been diagnosed as being at the same progressive or regressive stage of cancer,

wherein the comparison from step b) allows the determination of the stage of cancer progression or regression in an individual.

14. A method of diagnosing or prognosing cancer in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual, wherein said one or more gene transcripts corresponds to said one or more markers of claim 1 and claim 2, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having cancer,

c) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having cancer,

d) determining whether the level of said one or more gene transcripts of step a) classify with the levels of said transcripts in step b) as compared with levels of said transcripts in step c),

wherein said determination is indicative of said individual of step a) having cancer.

15. A method of determining a stage of disease progression or regression in an individual having a stage of cancer, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual having said stage of cancer, wherein said one or more gene transcripts

correspond to said one or more markers of claim 3 and claim 4, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having said stage of cancer,

c) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having said stage of cancer,

d) determining whether the level of said one or more gene transcripts of step a) classify with the levels of said transcripts in step b) as compared with levels of said transcripts in step c),

wherein said determination is indicative of said individual of step a) having said stage of cancer.

16. The method of any one of claims 1 - 4 and 11 - 15, wherein said one or more gene transcripts are transcribed from one or more genes selected from the group consisting of:

a) non-immune response genes,

b) genes expressed by non blood tissue, and

c) genes expressed by non lymphoid tissue.

17. The method of any one of claims 11 - 15, wherein said cancer is selected from the group consisting of liver cancer, bladder cancer, colon cancer, lung cancer, leukemia, ovarian cancer, cervical cancer, gastric cancer, kidney cancer, brain cancer, prostate cancer, pancreatic cancer, nasopharyngeal cancer, and breast cancer.

18. The method of claim 17 wherein said cancer is non-metastatic.

19. The method of any one of claims 11 - 15, wherein said one or more gene transcripts are transcribed from one or more genes selected from the group consisting of the genes listed in Table 3J, Table 3K and Table 3X.

20. The method of any one of claims 1 - 4 and 11 - 15, wherein said blood comprises a blood sample obtained from said one or more individuals.

21. The method of claim 20, wherein said blood sample consists of whole blood.

22. The method of claim 20, wherein said blood sample consists of a drop of blood.

23. The method of claim 20, wherein said blood sample consists of blood that has been lysed.

24. The method of claim 20, further comprising the step of isolating RNA from said blood samples.

25. The method of any one of claims 1 - 4 and 11 - 15, wherein the step of determining the level of each of said one or more gene transcripts comprises quantitative RT-PCR (QRT-PCR), wherein said one or more transcripts are from step a) and/or step b) of claims 1 - 4 and 11 - 15.

26. The method of claim 25, wherein said QRT-PCR comprises primers which hybridize to said one or more transcripts or the complement thereof, wherein said one or more transcripts are from step a) and/or step b) of claims 1 - 4 and 11 - 15.

27. The method of claim 26, wherein said primers are 15-25 nucleotides in length.

28. The method of claim 26, wherein said primers hybridize to one or more genes selected from the group of genes listed in Table 3J, Table 3K and Table 3X, or the complement thereof.

29. The method of any one of claims 1 - 4 and 11 - 15, wherein the step of determining the level of each of said one or more gene transcripts comprises hybridizing a first plurality of isolated nucleic acid molecules that correspond to said one or more transcripts, to an array comprising a second plurality of isolated nucleic acid molecules.

30. The method of claim 29, wherein said first plurality of isolated nucleic acid molecules comprises RNA, DNA, cDNA, PCR products or ESTs.

31. The method of claim 29, wherein said array comprises a plurality of isolated nucleic acid molecules comprising RNA, DNA, cDNA, PCR products or ESTs.

32. The method of claim 31, wherein said array comprises two or more of the markers of claim 1.

33. The method of claim 31, wherein said array comprises two or more of the markers of claim 2.

34. The method of claim 31, wherein said array comprises two or more of the markers of claim 3.

35. The method of claim 31, wherein said array comprises two or more of the markers of claim 4.

36. The method of claim 31, wherein said array comprises a plurality of nucleic acid molecules that correspond to genes of the human genome.

37. The method of claim 31, wherein said array comprises a plurality of nucleic acid molecules that correspond to two or more genes selected from the group consisting of the genes listed in Table 3J, Table 3K or Table 3X.

38. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 1.

39. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 2.

40. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 3.

41. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 4.

42. The method of claim 30, wherein said ESTs comprise at least 100 nucleotides in length.

43. An array consisting essentially of the plurality of nucleic acid molecules of claim 38.

44. An array consisting essentially of the plurality of nucleic acid molecules of claim 39.

45. An array consisting essentially of the plurality of nucleic acid molecules of claim 40.

46. An array consisting essentially of the plurality of nucleic acid molecules of claim 41.

47. A kit for diagnosing or prognosing cancer comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene selected from the group consisting of the markers of claim 1, claim 2, claim 3 and claim 4; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity,

c) an enzyme with thermostable DNA polymerase activity, and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

48. A kit for monitoring a course of therapeutic treatment of cancer, comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene selected from the group consisting of the markers of claim 1, claim 2, claim 3 and claim 4; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity,

c) an enzyme with thermostable DNA polymerase activity, and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

49. A kit for monitoring progression or regression of cancer, comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene selected from the group consisting of the markers of claim 1,

claim 2, claim 3 and claim 4; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity,

c) an enzyme with thermostable DNA polymerase activity, and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

50. The kit of any one of claims 47 - 49 wherein said gene-specific priming means is complementary to a gene selected from the group consisting of the genes listed in Table 3J, Table 3K and Table 3X.

51. A plurality of nucleic acid molecules that identify or correspond to two or more genes selected from the group consisting of the genes listed in Table 3J, Table 3K and Table 3X.

52. The method of claim 31, wherein said ESTs comprise at least 100 nucleotides in length.